

Yokota Sequence  
SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION NARA INSTITUTE OF SCIENCE  
AND TECHNOLOGY  
RESEARCH INSTITUTE OF INNOVATIVE TECHNOLOGY FOR THE EARTH  
KINKI UNIVERSITY  
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SHIGEOKA, Shigeru  
TOMIZAWA, Ken-ichi

<120> METHOD FOR IMPROVING PRODUCTIVITY OF PLANT BY CHLOROPLAST  
TECHNOLOGY

<130> 2006\_1303A

<140> US 10/591,752

<141> 2006-09-01

<150> PCT/JP2005/004037

<151> 2005-03-02

<150> JP 2004-059513

<151> 2004-03-03

<160> 18

<170> PatentIn version 3.4

<210> 1

<211> 358

<212> PRT

<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

<400> 1

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Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met  
20 25 30

Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser  
35 40 45

Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser  
50 55 60

Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln  
65 70 75 80

Lys Lys Leu Asp Val Val Ser Asn Glu Val Phe Ser Ser Cys Leu Arg  
85 90 95

# Yokota Sequence

Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro  
100 105 110

Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp  
115 120 125

Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser  
130 135 140

Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp  
145 150 155 160

His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val  
165 170 175

Asn Val Cys Gln Pro Gly Asp Asn Leu Leu Ala Ala Gly Tyr Cys Met  
180 185 190

Tyr Ser Ser Ser Val Ile Phe Val Leu Thr Ile Gly Lys Gly Val Tyr  
195 200 205

Ala Phe Thr Leu Asp Pro Met Tyr Gly Glu Phe Val Leu Thr Ser Glu  
210 215 220

Lys Ile Gln Ile Pro Lys Ala Gly Lys Ile Tyr Ser Phe Asn Glu Gly  
225 230 235 240

Asn Tyr Lys Met Trp Asp Asp Lys Leu Lys Lys Tyr Met Asp Asp Leu  
245 250 255

Lys Glu Pro Gly Glu Ser Gln Lys Pro Tyr Ser Ser Arg Tyr Ile Gly  
260 265 270

Ser Leu Val Gly Asp Phe His Arg Thr Leu Leu Tyr Gly Gly Ile Tyr  
275 280 285

Gly Tyr Pro Arg Asp Ala Lys Ser Lys Asn Gly Lys Leu Arg Leu Leu  
290 295 300

Tyr Glu Cys Ala Pro Met Ser Phe Ile Val Glu Gln Ala Gly Gly Lys  
305 310 315 320

Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile  
325 330 335

His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys  
340 345 350

# Yokota Sequence

Leu Glu Lys Tyr Leu Ala  
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<211> 1074  
<212> DNA  
<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

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accatcgttc tttctagcat ttcattggct tgtaaacaaa ttgcttcctt ggttcaacga 180  
gctggtatatt ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag 240  
aagaaacttg atgttgctc caatgaggtg ttttcgagct gcttgagatc gagtgggaaga 300  
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ggaaactata ttgttggtg ttgatccactt gatggttcatt ccaacattga tgcagctgtc 420  
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<210> 3  
<211> 333  
<212> PRT  
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1, 7-bisphosphatase

# Yokota Sequence

<400> 3

Val Asn Lys Ala Lys Asn Ser Ser Leu Val Thr Lys Cys Glu Leu Gly  
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Asp Ser Leu Glu Glu Phe Leu Ala Lys Ala Thr Thr Asp Lys Gly Leu  
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Ile Arg Leu Met Met Cys Met Gly Glu Ala Leu Arg Thr Ile Gly Phe  
35 40 45

Lys Val Arg Thr Ala Ser Cys Gly Gly Thr Gln Cys Val Asn Thr Phe  
50 55 60

Gly Asp Glu Gln Leu Ala Ile Asp Val Leu Ala Asp Lys Leu Leu Phe  
65 70 75 80

Glu Ala Leu Asn Tyr Ser His Phe Cys Lys Tyr Ala Cys Ser Glu Glu  
85 90 95

Leu Pro Glu Leu Gln Asp Met Gly Gly Pro Val Asp Gly Gly Phe Ser  
100 105 110

Val Ala Phe Asp Pro Leu Asp Gly Ser Ser Ile Val Asp Thr Asn Phe  
115 120 125

Ser Val Gly Thr Ile Phe Gly Val Trp Pro Gly Asp Lys Leu Thr Gly  
130 135 140

Val Thr Gly Arg Asp Gln Val Ala Ala Ala Met Gly Ile Tyr Gly Pro  
145 150 155 160

Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu  
165 170 175

Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr  
180 185 190

Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr  
195 200 205

Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu  
210 215 220

Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln  
225 230 235 240

Yokota Sequence

Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr  
245 250 255

Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe  
260 265 270

Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val  
275 280 285

Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr  
290 295 300

Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser  
305 310 315 320

Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala  
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<210> 4  
<211> 999  
<212> DNA  
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1,7-bisphosphatase

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gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggtgg aactcaatgt	180
gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttcttttc	240
gaggcattga actattcaca cttctgcaag tatgcttggt cagaagaact ccctgagctt	300
caagatatgg gagggcccggt tgatggcgga ttcagtgtag catttgaccc cttgatgga	360
tccagcattg tcgataccaa tttctcagtt gggaccatat tcggggtttg gccagggtgac	420
aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggctct	480
aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttcttctt	540
gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc	600
tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac	660
tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgtaaccag	720
atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag	780
ttgagggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tgggtggtcac	840

Yokota Sequence

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agcagtgagg gaaccaagtc tgtgttggac attgaagtca aaaaccttga tgacagaacc      900
caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc      960
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<210> 5  
 <211> 356  
 <212> PRT  
 <213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from  
 Synechococcus PCC 7942

<400> 5

Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala  
 1 5 10 15

Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala  
 20 25 30

Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu  
 35 40 45

Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro  
 50 55 60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys  
 65 70 75 80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val  
 85 90 95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser  
 100 105 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro  
 115 120 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys  
 130 135 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu  
 145 150 155 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg  
 165 170 175

# Yokota Sequence

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg  
180 185 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly  
195 200 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro  
210 215 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe  
225 230 235 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile  
245 250 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile  
260 265 270

Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln  
275 280 285

Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu  
290 295 300

Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile  
305 310 315 320

Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe  
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Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp  
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Arg Pro Glu Arg  
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<210> 6  
<211> 1312  
<212> DNA  
<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from  
Synechococcus PCC 7942

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Yokota Sequence			
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tgtttttcag cgaatccatt tgcgatcgtc tttcaaacc ttttttcgtc aaccttcttt	1260		
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 <211> 133  
 <212> DNA  
 <213> Nicotiana tabacum

<220>

<223> psbA promoter

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aagccttcca ttttctatct tgattttag aaaactagtg tgcttgggag tccctgatga	120
ttaaataaac caa	133

<210> 8  
 <211> 159



# Yokota Sequence

<212> DNA  
<213> *Nicotiana tabacum*

<220>

<223> rps16 terminator

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atttgtattt ttttatcatt gcttccattg aattactag 159

<210> 9  
<211> 805  
<212> DNA  
<213> *Escherichia coli*

<220>

<223> aadA

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tggatggcgg cctgaagcca cacagtata ttgatttgct gggtacggtg accgtaaggc 180  
ttgatgaaac aacgcggcga gctttgatca acgacctttt ggaaacttcg gcttcccctg 240  
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cccagtatca gcccgtcata cttgaagcta gacaggctta tcttggacaa gaagaagatc 720  
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<213> Artificial sequence

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<223> synthetic construct

# Yokota Sequence

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<223> pLD6

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# Yokota Sequence

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Yokota Sequence

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<220>  
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 <213> Nicotiana tabacum

<220>  
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Yokota Sequence  
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acaaattgac ttattatact cctgagtacc aaaccaagga tactgatata ttggcagcat 540  
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Yokota Sequence

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# Yokota Sequence

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Yokota Sequence

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 <212> DNA  
 <213> Nicotiana tabacum

<220>  
 <223> rbcL

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Yokota Sequence

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 <223> accD

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# Yokota Sequence

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21

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<220>  
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<400> 18  
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7